STIC-Biotech/ChemLib 1704463

From: Russel, Jeffrey
Sent: Wednesday, November 02, 2005 3:43 PM
To: STIC-Biotech/ChemLib
Subject: Database Search Request

Requester:
Jeffrey Russel (TC1600)
Art Unit:
1654
Employee Number:
62785
Office Location:
REM 3D19
Phone_Number:
571-272-0969
Mailbox Number:
REM 3C18

Checked JR 11-14-2005

Case serial number:
10/810,578
Class / Subclass(es):
NA
Earliest Priority Filing Date:
NA
Format preferred for results:
Diskette
Search Topic Information:
Please search SEQ ID NO:7 (KEEPPAPPQSP) in STN, in the U.S. patent application sequence database (pending, published, and issued), and in Geneseq/Uniprot/PIR. Thank you.
Special Instructions and Other Comments:

Point of Contact:
Alexandra Waclawiw
Technical Info. Specialist
CM1 6A02 Tel 308-4447

****
Searcher:_____
Searcher Phone:_____
Date Searcher Picked up: 11-3
Date completed: 10 11-3-05
Searcher Prep Time:_____
Online Time: 10

****
Type of Search
NA#_____ AA#: 1
S/L:_____ Oligomer:_____
Encode/Transl:_____
Structure #:_____Text:____
Inventor:_____ Litigation:___

****
Vendors and cost where applicable
STN:_____
DIALOG:_____
QUESTEL/ORBIT:_____
LEXIS/NEXIS:_____
SEQUENCE SYSTEM:_____
WWW/Internet:_____
Other (Specify):_____

```
=> d his ful

     (FILE 'HOME' ENTERED AT 09:30:44 ON 03 NOV 2005)

     FILE 'REGISTRY' ENTERED AT 09:30:50 ON 03 NOV 2005

     FILE 'REGISTRY' ENTERED AT 09:31:23 ON 03 NOV 2005
L1             2 SEA ABB=ON  PLU=ON  KEEPPAPPQSP/SQSP

     FILE 'CAPLUS' ENTERED AT 09:31:43 ON 03 NOV 2005
L2             4 SEA ABB=ON  PLU=ON  L1
                 D SC
                 D SCAN TI


     FILE HOME

     FILE REGISTRY
     Property values tagged with IC are from the ZIC/VINITI data file
     provided by InfoChem.

     STRUCTURE FILE UPDATES:     1 NOV 2005  HIGHEST RN 866526-24-1
     DICTIONARY FILE UPDATES:    1 NOV 2005  HIGHEST RN 866526-24-1

     New CAS Information Use Policies, enter HELP USAGETERMS for details.

     TSCA INFORMATION NOW CURRENT THROUGH JULY 14, 2005

       Please note that search-term pricing does apply when
       conducting SmartSELECT searches.

     ************************************************************
     *                                                          *
     * The CA roles and document type information have been removed from *
     * the IDE default display format and the ED field has been added,   *
     * effective March 20, 2005.  A new display format, IDERL, is now    *
     * available and contains the CA role and document type information. *
     *                                                          *
     ************************************************************

     Structure search iteration limits have been increased.  See HELP SLIMITS
     for details.

     REGISTRY includes numerically searchable data for experimental and
     predicted properties as well as tags indicating availability of
     experimental property data in the original document.  For information
     on property searching in REGISTRY, refer to:

     http://www.cas.org/ONLINE/UG/regprops.html

     FILE CAPLUS

     Copyright of the articles to which records in this database refer is
     held by the publishers listed in the PUBLISHER (PB) field (available
     for records published or updated in Chemical Abstracts after December
     26, 1996), unless otherwise indicated in the original publications.
     The CA Lexicon is the copyrighted intellectual property of the
     American Chemical Society and is provided to assist you in searching
     databases on STN.  Any dissemination, distribution, copying, or storing
```

FILE COVERS 1907 - 3 Nov 2005 VOL 143 ISS 19
FILE LAST UPDATED: 2 Nov 2005 (20051102/ED)

Effective October 17, 2005, revised CAS Information Use Policies apply. They are available for your review at:

http://www.cas.org/infopolicy.html

```
=> fil reg
FILE 'REGISTRY' ENTERED AT 09:32:25 ON 03 NOV 2005
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
PLEASE SEE "HELP USAGETERMS" FOR DETAILS.
COPYRIGHT (C) 2005 American Chemical Society (ACS)

Property values tagged with IC are from the ZIC/VINITI data file
provided by InfoChem.

STRUCTURE FILE UPDATES:     1 NOV 2005  HIGHEST RN 866526-24-1
DICTIONARY FILE UPDATES:    1 NOV 2005  HIGHEST RN 866526-24-1

New CAS Information Use Policies, enter HELP USAGETERMS for details.

TSCA INFORMATION NOW CURRENT THROUGH JULY 14, 2005

  Please note that search-term pricing does apply when
  conducting SmartSELECT searches.

**********************************************************************
*                                                                    *
* The CA roles and document type information have been removed from *
* the IDE default display format and the ED field has been added,    *
* effective March 20, 2005.  A new display format, IDERL, is now     *
* available and contains the CA role and document type information.  *
*                                                                    *
**********************************************************************

Structure search iteration limits have been increased.  See HELP SLIMITS
for details.

REGISTRY includes numerically searchable data for experimental and
predicted properties as well as tags indicating availability of
experimental property data in the original document.  For information
on property searching in REGISTRY, refer to:

http://www.cas.org/ONLINE/UG/regprops.html

=> d que l1
L1            2 SEA FILE=REGISTRY ABB=ON  PLU=ON  KEEPPAPPQSP/SQSP


=> d l1 sqide3 1-2

L1   ANSWER 1 OF 2  REGISTRY  COPYRIGHT 2005 ACS on STN
RN   583028-61-9  REGISTRY
CN   L-Proline, L-lysyl-L-α-glutamyl-L-α-glutamyl-L-prolyl-L-prolyl-
     L-alanyl-L-prolyl-L-prolyl-L-glutaminyl-L-seryl- (9CI)  (CA INDEX NAME)
OTHER NAMES:
CN   10: PN: WO2004052404 SEQID: 10 unclaimed sequence
FS   PROTEIN SEQUENCE; STEREOSEARCH
SQL  11

PATENT ANNOTATIONS (PNTE):
Sequence |Patent
Source   |Reference
=========+============
Not Given|WO2004052404
```

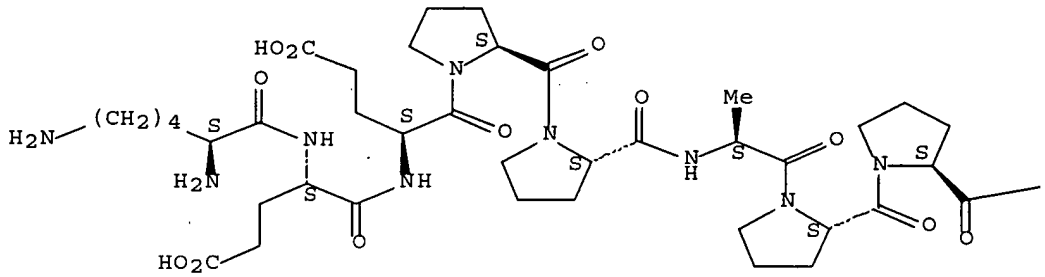
|unclaimed
|SEQID 10

SEQ3 1 Lys-Glu-Glu-Pro-Pro-Ala-Pro-Pro-Gln-Ser-
=== === === === === === === === === ===
11 Pro
===
HITS AT: 1-11

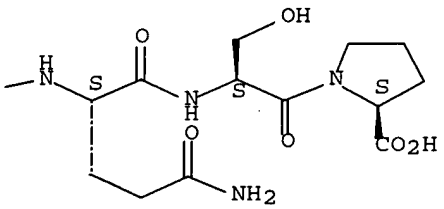
RELATED SEQUENCES AVAILABLE WITH SEQLINK
MF C52 H81 N13 O18
SR CA
LC STN Files: CA, CAPLUS
DT.CA CAplus document type: Journal; Patent
RL.P Roles from patents: PRP (Properties)
RL.NP Roles from non-patents: BIOL (Biological study); USES (Uses)

Absolute stereochemistry.

PAGE 1-A



PAGE 1-B



PROPERTY DATA AVAILABLE IN THE 'PROP' FORMAT

2 REFERENCES IN FILE CA (1907 TO DATE)
2 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L1 ANSWER 2 OF 2 REGISTRY COPYRIGHT 2005 ACS on STN
RN 348089-26-9 REGISTRY

CN L-Proline, L-lysyl-L-α-glutamyl-L-α-glutamyl-L-prolyl-L-prolyl-L-alanyl-L-prolyl-L-prolyl-L-glutaminyl-O-phosphono-L-seryl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 7: PN: US20020147146 SEQID: 7 claimed protein
CN 7: PN: WO0149709 SEQID: 7 claimed protein
CN 8: PN: WO2004052404 SEQID: 8 claimed protein
FS PROTEIN SEQUENCE; STEREOSEARCH
SQL 11
NTE modified (modifications unspecified)

type	------ location ------		description
modification	Ser-10	-	phosphono<PO2>

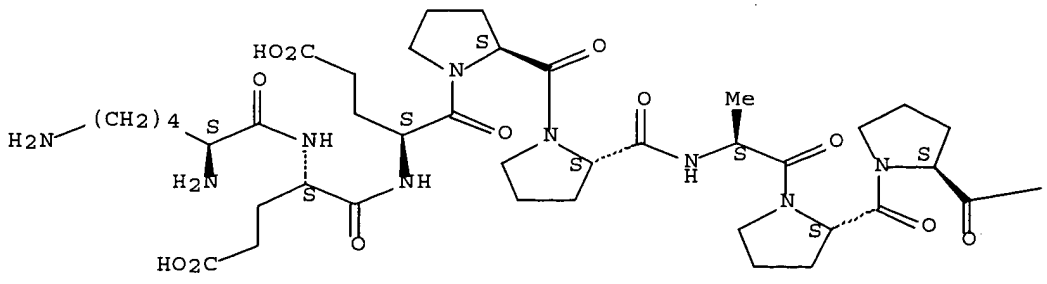
PATENT ANNOTATIONS (PNTE):

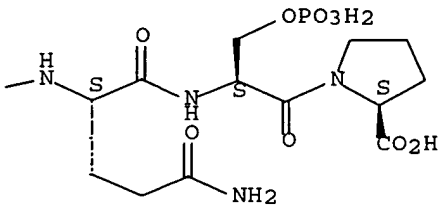
Sequence Source	Patent Reference
Not Given	WO2001049709 claimed SEQID 7

SEQ3 1 Lys-Glu-Glu-Pro-Pro-Ala-Pro-Pro-Gln-Ser-
=== === === === === === === === === ===
11 Pro
===
HITS AT: 1-11

RELATED SEQUENCES AVAILABLE WITH SEQLINK
MF C52 H82 N13 O21 P
SR CA
LC STN Files: CA, CAPLUS, USPAT2, USPATFULL
DT.CA CAplus document type: Journal; Patent
RL.P Roles from patents: BIOL (Biological study); PREP (Preparation); PROC (Process); PRP (Properties); USES (Uses)
RL.NP Roles from non-patents: BIOL (Biological study); USES (Uses)

Absolute stereochemistry.





4 REFERENCES IN FILE CA (1907 TO DATE)
4 REFERENCES IN FILE CAPLUS (1907 TO DATE)

=> fil caplus
FILE 'CAPLUS' ENTERED AT 09:32:38 ON 03 NOV 2005
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
PLEASE SEE "HELP USAGETERMS" FOR DETAILS.

FILE COVERS 1907 - 3 Nov 2005 VOL 143 ISS 19
FILE LAST UPDATED: 2 Nov 2005 (20051102/ED)

Effective October 17, 2005, revised CAS Information Use Policies apply. They are available for your review at:

http://www.cas.org/infopolicy.html
'OBI' IS DEFAULT SEARCH FIELD FOR 'CAPLUS' FILE

=> d que l2
L1 2 SEA FILE=REGISTRY ABB=ON PLU=ON KEEPPAPPQSP/SQSP
L2 4 SEA FILE=CAPLUS ABB=ON PLU=ON L1

=> d .ca l2 1-4

L2 ANSWER 1 OF 4 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2004:513566 CAPLUS Full-text
DOCUMENT NUMBER: 141:47343
TITLE: Glycogen synthase kinase-3 inhibitors
INVENTOR(S): Eldar-Finkelman, Hagit
PATENT ASSIGNEE(S): Tel Aviv University Future Technology Development L.P., Israel
SOURCE: PCT Int. Appl., 95 pp.

CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2004052404	A2	20040624	WO 2003-IL1057	20031211
WO 2004052404	A3	20040729		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW				
RW: BW, GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
CA 2509374	AA	20040624	CA 2003-2509374	20031211
EP 1569956	A2	20050907	EP 2003-777156	20031211
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, SK				

PRIORITY APPLN. INFO.:
US 2002-432644P P 20021212
US 2003-482719P P 20030627
WO 2003-IL1057 W 20031211

OTHER SOURCE(S): MARPAT 141:47343
ED Entered STN: 25 Jun 2004
AB Novel conjugates that are capable of inhibiting GSK-3 activity, a process of producing same, pharmaceutical compns. including same and methods of using same in the treatment of GSK-3 mediated conditions are disclosed. Methods of treating affective disorders using GSK-3 inhibitors are further disclosed.
IC ICM A61K047-48
CC 1-10 (Pharmacology)
Section cross-reference(s): 2, 63
IT 348089-22-5 348089-26-9 348089-28-1 348089-33-8
706785-92-4 706785-93-5
RL: PAC (Pharmacological activity); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(glycogen synthase kinase-3 inhibitors)
IT 149155-45-3 348089-31-6 464875-01-2 583028-61-9
583028-62-0 583028-63-1 708270-79-5 708270-80-8 708270-82-0
708270-83-1 708270-84-2 708270-85-3
RL: PRP (Properties)
(unclaimed sequence; glycogen synthase kinase-3 inhibitors)

L2 ANSWER 2 OF 4 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2003:420432 CAPLUS Full-text
DOCUMENT NUMBER: 139:191139
TITLE: Insulin mimetic action of synthetic phosphorylated peptide inhibitors of glycogen synthase kinase-3
AUTHOR(S): Plotkin, Batya; Kaidanovich, Oksana; Talior, Ilana; Eldar-Finkelman, Hagit
CORPORATE SOURCE: Department of Human Genetics and Molecular Medicine, Institute of Molecular Medicine, Sackler School of Medicine, Tel Aviv University, Tel Aviv-Jaffa, Israel
SOURCE: Journal of Pharmacology and Experimental Therapeutics (2003), 305(3), 974-980
CODEN: JPETAB; ISSN: 0022-3565

PUBLISHER: American Society for Pharmacology and Experimental Therapeutics
DOCUMENT TYPE: Journal
LANGUAGE: English
ED Entered STN: 02 Jun 2003
AB Glycogen synthase kinase-3 (GSK-3) was shown to be a key factor in attenuation of the cellular action of insulin. The authors speculated that inhibition of GSK-3 might have a potential therapeutic value in treatment of insulin resistance and type 2 diabetes. Here, the authors present a novel class of specific phosphorylated peptide inhibitors of GSK-3, which in sharp contrast to other protein kinase inhibitors that are ATP analogs, are substrate-competitive. The authors show that the GSK-3 peptide inhibitor activated glycogen synthase activity 2.5-fold in human embryonic kidney 293 cells, and increased glucose uptake in primary mouse adipocytes in the absence or presence of insulin compared with cells treated with two resp. peptide controls. In addition, an i.p. administration of GSK-3 peptide inhibitor to normal or insulin-resistant obese C57BL/6J mice, improved their performance on glucose tolerance tests compared with control-treated animals. The authors present here a novel rational strategy for developing specific GSK-3 inhibitors and point toward GSK-3 as a promising therapeutic target in insulin resistance and type-2 diabetes.
CC 1-10 (Pharmacology)
Section cross-reference(s): 2
IT 158198-86-8 348089-18-9 348089-20-3 348089-22-5 348089-26-9
348089-28-1 348089-31-6 348089-33-8 464875-01-2 583028-59-5
583028-60-8 583028-61-9 583028-62-0 583028-63-1
RL: BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(insulin mimetic action of synthetic phosphorylated peptide inhibitors of glycogen synthase kinase-3)
REFERENCE COUNT: 43 THERE ARE 43 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 3 OF 4 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2002:778705 CAPLUS Full-text
DOCUMENT NUMBER: 137:304805
TITLE: Glycogen synthase kinase-3 inhibitor peptides, inhibitor design, and therapeutic use
INVENTOR(S): Eldar-Finkelman, Hagit
PATENT ASSIGNEE(S): Ramot University Authority for Applied Research & Industrial Development Ltd., Israel; Tel Aviv University Future Technology Development L.P.
SOURCE: U.S. Pat. Appl. Publ., 34 pp., Cont.-in-part of Appl. No. PCT/US01/00123.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2002147146	A1	20021010	US 2001-951902	20010914
US 6780625	B2	20040824		
WO 2001049709	A1	20010712	WO 2001-US123	20010103

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN,

YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

US 2004162234	A1	20040819	US 2004-810578		20040329
PRIORITY APPLN. INFO.:			US 2000-174308P	P	20000103
			US 2000-206115P	P	20000522
			WO 2001-US123	A2	20010103
			US 2001-951902	A3	20010914

ED Entered STN: 11 Oct 2002

AB Peptide inhibitors of glycogen synthase kinase-3 (GSK-3) have an amino acid sequence motif of XZXXXS(p)X [S(p) = phosphorylated serine, phosphorylated threonine; X = any amino acid; Z = any amino acid except serine or threonine]. These inhibitors, which are about 7-50 amino acids long, are specific for GSK-3 and strongly inhibit the enzyme with an IC50 of about 150 μM. Also provided are methods of treating biol. conditions mediated by GSK-3 activity, such as potentiating insulin signaling in a subject, treating or preventing type 2 diabetes in a patient, and treating Alzheimer's Disease by administering peptide inhibitors. Compns. of these peptide inhibitors and pharmaceutically acceptable carriers are also provided, as is a method for identifying inhibitors of GSK-3. The invention further relates to a computer-assisted method of structure based drug design of GSK-3 inhibitors using a three-dimensional structure of a peptide substrate of GSK-3.

IC ICM A61K038-17
ICS C12N009-99
INCL 514012000
CC 1-12 (Pharmacology)
Section cross-reference(s): 63
IT 348089-22-5P 348089-26-9P 348089-28-1P
RL: PAC (Pharmacological activity); PRP (Properties); SPN (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(glycogen synthase kinase-3 inhibitors, inhibitor design, and therapeutic use)
REFERENCE COUNT: 80 THERE ARE 80 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 4 OF 4 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2001:507722 CAPLUS Full-text
DOCUMENT NUMBER: 135:87200
TITLE: Glycogen synthase kinase-3 inhibitors
INVENTOR(S): Eldar-Finkleman, Hagit
PATENT ASSIGNEE(S): Ramot University Authority for Applied Research & Industrial Development Ltd., Israel; McInnis, Patricia A.
SOURCE: PCT Int. Appl., 49 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001049709	A1	20010712	WO 2001-US123	20010103

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN,

YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

US 2002147146	A1	20021010	US 2001-951902	20010914
US 6780625	B2	20040824		
US 2004162234	A1	20040819	US 2004-810578	20040329

PRIORITY APPLN. INFO.:

US 2000-174308P	P	20000103
US 2000-206115P	P	20000522
WO 2001-US123	A2	20010103
US 2001-951902	A3	20010914

ED Entered STN: 13 Jul 2001

AB The invention is directed to a highly effective and specific peptide inhibitors of glycogen synthase kinase-3 (GSK-3) and useful implications of these peptides. The peptide inhibitors of the invention include therewithin the amino acid motif XZXXXS (p)X, where S(p)=phosphorylated serine or phosphorylated threonine, X=any amino acid, and Z=any amino acid except serine, or threonine. The peptides competitively bind to GSK-3 in vitro with high affinity. Because the amino acid Z in the motif is not phosphorylated, the peptide inhibitor cannot be phosphorylated. Thus, the peptide inhibits the catalytic activity of GSK-3, since the enzyme cannot proceed to phosphorylate other proteins. The peptide inhibitors can be used to diseases mediated by GSK-3 activity such as non-insulin-dependent diabetes mellitus or Alzheimer's disease.

IC ICM C07K007-06
ICS C12N009-12

CC 1-12 (Pharmacology)
Section cross-reference(s): 7

IT 149155-45-3 158198-86-8 348089-18-9 348089-20-3 348089-22-5 348089-24-7 348089-26-9 348089-28-1 348089-30-5 348089-31-6 348089-33-8
RL: BAC (Biological activity or effector, except adverse); BPR (Biological process); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); PROC (Process); USES (Uses)
(peptide glycogen synthase kinase-3 inhibitors and their use in treating diseases such as non-insulin-dependent diabetes mellitus and Alzheimer's disease)

REFERENCE COUNT: 7 THERE ARE 7 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

=>

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 3, 2005, 08:51:21 ; Search time 171 Seconds
(without alignments)
32.941 Million cell updates/sec

Title: US-10-810-578-7
Perfect score: 63
Sequence: 1 KEEPPAPPQSP 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	60	95.2	213	2	Q7YR98	Q7yr98 bos taurus
2	60	95.2	529	1	HSF1_HUMAN	Q00613 homo sapien
3	55	87.3	448	2	Q63717	Q63717 rattus norv
4	52	82.5	525	1	HSF1_MOUSE	P38532 mus musculu
5	49	77.8	231	2	Q6ASV2	Q6asv2 oryza sativ
6	49	77.8	387	2	Q8HXU1	Q8hxu1 priodontes
7	49	77.8	407	2	Q95KU3	Q95ku3 cabassous u
8	48.5	77.0	562	2	Q8NAF0	Q8naf0 homo sapien
9	48.5	77.0	562	2	Q80VM4	Q80vm4 mus musculu
10	48	76.2	491	1	HSF1_CHICK	P38529 gallus gall
11	47	74.6	94	2	Q8MVN0	Q8mvn0 boltenia vi
12	47	74.6	153	2	Q9NA70	Q9na70 caenorhabdi
13	47	74.6	432	2	Q9ESV6	Q9esv6 rattus norv
14	47	74.6	543	1	CH60_BACFO	P81284 bacteroides
15	47	74.6	561	2	Q90711	Q90711 gallus gall

16	47	74.6	706	2	Q7RXM5	Q7rxm5 neurospora
17	47	74.6	1219	2	Q90710	Q90710 gallus gall
18	46	73.0	224	2	Q9CRT7	Q9crt7 mus musculu
19	46	73.0	254	1	WAPA_BACST	P42018 bacillus st
20	46	73.0	276	2	Q7MCR3	Q7mcr3 vibrio vuln
21	46	73.0	282	2	Q9ZR24	Q9zr24 perilla fru
22	46	73.0	297	1	RPOF_STRAU	P37970 streptomyce
23	46	73.0	303	2	Q9D116	Q9d116 mus musculu
24	46	73.0	303	2	Q8R3W0	Q8r3w0 mus musculu
25	46	73.0	319	2	Q8BP27	Q8bp27 mus musculu
26	46	73.0	319	2	Q9D0D7	Q9d0d7 mus musculu
27	46	73.0	319	2	Q9D4W4	Q9d4w4 m mus muscu
28	46	73.0	348	2	Q9CKT8	Q9ckt8 pasteurella
29	46	73.0	377	2	Q6T3V3	Q6t3v3 ctenopharyn
30	46	73.0	471	2	Q8NCK7	Q8nck7 homo sapien
31	46	73.0	699	2	Q6YI93	Q6yi93 xenopus lae
32	46	73.0	724	2	Q94BX5	Q94bx5 arabidopsis
33	46	73.0	724	2	Q6R3K4	Q6r3k4 arabidopsis
34	46	73.0	760	1	MR11_NEUCR	Q9c291 neurospora
35	46	73.0	763	2	Q9XDH2	Q9xdh2 mycobacteri
36	46	73.0	803	2	Q9SX70	Q9sx70 arabidopsis
37	45	71.4	317	2	Q64812	Q64812 autographa
38	45	71.4	389	2	Q8G537	Q8g537 bifidobacte
39	45	71.4	412	2	Q8HXT9	Q8hxt9 tolypeutes
40	45	71.4	422	2	Q8FLQ8	Q8flq8 corynebacte
41	45	71.4	433	2	Q7SYN6	Q7syn6 brachydanio
42	45	71.4	433	2	Q9PT91	Q9pt91 brachydanio
43	45	71.4	461	2	Q7ZWI6	Q7zwi6 brachydanio
44	45	71.4	469	2	Q9V3B8	Q9v3b8 drosophila
45	45	71.4	482	2	Q9LZC9	Q9lzc9 arabidopsis
46	45	71.4	490	2	Q8Y0Q4	Q8y0q4 ralstonia s
47	45	71.4	541	1	PTN5_MOUSE	P54830 mus musculu
48	45	71.4	541	2	Q8CAN0	Q8can0 mus musculu
49	45	71.4	581	2	Q80WU9	Q80wu9 mus musculu
50	45	71.4	670	2	Q8GX23	Q8gx23 arabidopsis
51	45	71.4	674	2	O65672	O65672 arabidopsis
52	45	71.4	681	2	Q9FFW5	Q9ffw5 arabidopsis
53	45	71.4	738	2	Q82YD4	Q82yd4 streptomyce
54	45	71.4	757	2	Q7SF38	Q7sf38 neurospora
55	45	71.4	805	2	O92431	O92431 bombyx mori
56	45	71.4	808	1	Y066_NPVAC	P41467 autographa
57	45	71.4	810	2	Q8B9I6	Q8b9i6 rachiplusia
58	45	71.4	859	2	Q9HFI9	Q9hfi9 neurospora
59	45	71.4	978	1	MCR_MOUSE	Q8vii8 mus musculu
60	45	71.4	981	1	MCR_RAT	P22199 rattus norv
61	45	71.4	1063	2	Q6X2U1	Q6x2u1 rubella vir
62	45	71.4	1063	2	Q6X2U3	Q6x2u3 rubella vir
63	45	71.4	1135	2	Q812E1	Q812e1 mus musculu
64	44	69.8	96	2	Q7S8X2	Q7s8x2 neurospora
65	44	69.8	128	2	Q852V9	Q852v9 mycobacteri
66	44	69.8	166	2	Q9UVD0	Q9uvd0 pneumocysti
67	44	69.8	299	2	Q89QQ7	Q89qq7 bradyrhizob
68	44	69.8	317	2	Q9D3N6	Q9d3n6 mus musculu
69	44	69.8	320	2	Q96BE1	Q96be1 homo sapien
70	44	69.8	322	2	Q6PIM1	Q6pim1 homo sapien
71	44	69.8	322	2	Q8K558	Q8k558 mus musculu
72	44	69.8	326	2	Q89I24	Q89i24 bradyrhizob

73	44	69.8	331	2	Q91640	Q91640 xenopus lae
74	44	69.8	356	2	Q75HC4	Q75hc4 oryza sativ
75	44	69.8	368	2	Q6TNR2	Q6tnr2 brachydanio
76	44	69.8	385	2	Q8HXU7	Q8hxu7 dasypus kap
77	44	69.8	388	2	Q9KIS6	Q9kis6 brucella ab
78	44	69.8	391	2	Q9RPX5	Q9rpx5 brucella su
79	44	69.8	391	2	Q8FXK6	Q8fxk6 brucella su
80	44	69.8	393	2	Q6BS91	Q6bs91 debaryomyce
81	44	69.8	411	2	Q95KU2	Q95ku2 dasypus nov
82	44	69.8	417	2	Q20203	Q20203 caenorhabdi
83	44	69.8	471	2	Q6KA29	Q6ka29 oryza sativ
84	44	69.8	478	2	Q9NXK1	Q9nxk1 homo sapien
85	44	69.8	492	2	Q6C3J1	Q6c3j1 yarrowia li
86	44	69.8	506	2	Q8PDA7	Q8pda7 xanthomonas
87	44	69.8	510	2	Q8I0Z6	Q8i0z6 caenorhabdi
88	44	69.8	536	2	O84053	O84053 chlamydia t
89	44	69.8	552	2	Q86YA9	Q86ya9 homo sapien
90	44	69.8	583	2	Q6YUS6	Q6yus6 oryza sativ
91	44	69.8	590	2	Q91VM4	Q91vm4 mus musculu
92	44	69.8	593	2	Q8I0Z5	Q8i0z5 caenorhabdi
93	44	69.8	596	2	Q9CVF3	Q9cvf3 mus musculu
94	44	69.8	623	2	Q82HC6	Q82hc6 streptomyce
95	44	69.8	639	1	GGA1_HUMAN	Q9ujy5 homo sapien
96	44	69.8	645	2	Q8VDN7	Q8vdn7 mus musculu
97	44	69.8	656	2	Q6IC75	Q6ic75 homo sapien
98	44	69.8	712	2	Q8RWX5	Q8rwx5 arabidopsis
99	44	69.8	722	1	Z219_HUMAN	Q9p2y4 homo sapien
100	44	69.8	722	2	Q8IYC1	Q8iyc1 homo sapien
101	44	69.8	726	2	Q66H48	Q66h48 rattus norv
102	44	69.8	726	2	Q6IQX8	Q6iqx8 mus musculu
103	44	69.8	756	2	Q8RP53	Q8rp53 streptococc
104	44	69.8	821	2	Q7SC46	Q7sc46 neurospora
105	44	69.8	839	2	Q69ZV6	Q69zv6 mus musculu
106	44	69.8	869	2	Q65ZC5	Q65zc5 caenorhabdi
107	44	69.8	882	2	Q80TZ9	Q80tz9 mus musculu
108	44	69.8	891	2	Q9VGJ8	Q9vgj8 drosophila
109	44	69.8	937	1	YM92_CAEEL	P34531 caenorhabdi
110	44	69.8	956	2	Q9LJ64	Q9lj64 arabidopsis
111	44	69.8	957	1	SLK5_MOUSE	Q810b7 mus musculu
112	44	69.8	958	1	SLK5_HUMAN	O94991 homo sapien
113	44	69.8	995	2	Q9Y2W4	Q9y2w4 homo sapien
114	44	69.8	1006	2	Q62901	Q62901 rattus norv
115	44	69.8	1012	2	O43393	O43393 homo sapien
116	44	69.8	1012	2	O75359	O75359 homo sapien
117	44	69.8	1025	2	Q6NQY8	Q6nqy8 drosophila
118	44	69.8	1026	1	STAU_DROME	P25159 drosophila
119	44	69.8	1026	2	Q9V8B9	Q9v8b9 drosophila
120	44	69.8	1114	2	Q6P9L3	Q6p9l3 mus musculu
121	44	69.8	1185	2	Q8VDF4	Q8vdf4 mus musculu
122	44	69.8	1296	2	O75046	O75046 homo sapien
123	44	69.8	1506	2	Q6P6B9	Q6p6b9 homo sapien
124	44	69.8	1566	2	Q9P2R6	Q9p2r6 homo sapien
125	44	69.8	1589	2	Q69ZQ7	Q69zq7 mus musculu
126	44	69.8	1634	2	Q6C908	Q6c908 yarrowia li
127	44	69.8	1651	2	Q80TC8	Q80tc8 mus musculu
128	44	69.8	2321	2	Q6R5R1	Q6r5r1 meleagrid h
129	44	69.8	2321	2	Q9DGT6	Q9dgt6 meleagrid h

130	44	69.8	2323	2	Q6HAA3	Q6haa3 meleagrid h
131	44	69.8	2999	2	Q8CHI7	Q8chi7 mus musculu
132	44	69.8	3035	2	Q8CHI8	Q8chi8 mus musculu
133	44	69.8	3084	2	Q8UZ11	Q8uz11 pseudorabie
134	44	69.8	4340	2	O30764	O30764 streptomyce
135	43	68.3	118	2	Q6K924	Q6k924 oryza sativ
136	43	68.3	133	2	Q65CJ9	Q65cj9 gallus gall
137	43	68.3	147	1	CHS1_HUMAN	Q9y2v2 homo sapien
138	43	68.3	147	1	CHS1_RAT	Q9wu49 rattus norv
139	43	68.3	163	2	Q9IGT7	Q9igt7 porcine ade
140	43	68.3	167	2	Q7XII6	Q7xii6 oryza sativ
141	43	68.3	167	2	Q73WI5	Q73wi5 mycobacteri
142	43	68.3	178	2	Q9H204	Q9h204 homo sapien
143	43	68.3	193	2	Q9BZJ5	Q9bzj5 homo sapien
144	43	68.3	221	2	Q9X8P1	Q9x8p1 streptomyce
145	43	68.3	222	2	Q9S740	Q9s740 arabidopsis
146	43	68.3	235	2	Q86H42	Q86h42 dictyosteli
147	43	68.3	267	2	Q6P5B3	Q6p5b3 mus musculu
148	43	68.3	315	2	Q66VY4	Q66vy4 gallus gall
149	43	68.3	323	1	PF27_MOUSE	P52875 mus musculu
150	43	68.3	323	2	Q21014	Q21014 caenorhabdi

ALIGNMENTS

```
RESULT 1
Q7YR98
ID   Q7YR98      PRELIMINARY;      PRT;   213 AA.
AC   Q7YR98;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Heat shock transcription factor 1 (Fragment).
GN   Name=HSF1;
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC   Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   PubMed=14667821; DOI=10.1016/S0888-7543(03)00238-6;
RA   Winter A., Alzinger A., Fries R.;
RT   "Assessment of the gene content of the chromosomal regions flanking
RT   bovine DGAT1.";
RL   Genomics 83:172-180(2004).
DR   EMBL; AJ518960; CAD58797.1; -.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006457; P:protein folding; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   GO; GO:0006986; P:response to unfolded protein; IEA.
DR   InterPro; IPR000232; HSF_DNA_bind.
DR   InterPro; IPR010542; Vert_HS_TF.
DR   Pfam; PF00447; HSF_DNA-bind; 1.
DR   Pfam; PF06546; Vert_HS_TF; 1.
```

```
KW   Heat shock.
FT   NON_TER       1      1
FT   NON_TER     213    213
SQ   SEQUENCE   213 AA;  22446 MW;  AB675AEA6FF3BA1A CRC64;

  Query Match             95.2%;  Score 60;  DB 2;  Length 213;
  Best Local Similarity   90.9%;  Pred. No. 5.3;
  Matches   10;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KEEPPAPPQSP 11
              |||||:|||||
Db        135 KEEPPSPPQSP 145


Search completed: November  3, 2005, 09:10:06
Job time : 185 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 3, 2005, 08:54:17 ; Search time 37 Seconds
(without alignments)
28.605 Million cell updates/sec

Title: US-10-810-578-7
Perfect score: 63
Sequence: 1 KEEPPAPPQSP 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	60	95.2	529	2	A41137	heat shock transcr
2	55	87.3	448	2	S52751	heat shock transcr
3	52	82.5	503	2	A40583	heat shock transcr
4	47	74.6	153	2	T31654	hypothetical prote
5	46	73.0	803	2	G96523	F11A17.8 [imported
6	45	71.4	482	2	T48384	hypothetical prote
7	45	71.4	674	2	T05264	probable serine/th
8	45	71.4	805	2	T41810	AcMNPV orf66 - Bom
9	45	71.4	808	2	C72858	AcOrf-66 protein -
10	45	71.4	929	2	T52517	hypothetical prote
11	45	71.4	981	2	A41401	mineralocorticoid
12	44	69.8	417	2	T22024	hypothetical prote
13	44	69.8	460	2	T31587	hypothetical prote

14	44	69.8	536	2	H71563	hypothetical prote
15	44	69.8	568	2	A34891	Ig heavy chain pre
16	44	69.8	597	2	S40998	hypothetical prote
17	44	69.8	609	2	T14759	hypothetical prote
18	44	69.8	893	2	G88551	protein M01A8.2 [i
19	44	69.8	1006	2	T42731	atrophin-1 related
20	44	69.8	1026	1	A40315	maternal effect pr
21	43	68.3	221	2	T36514	hypothetical prote
22	43	68.3	222	2	H96711	hypothetical prote
23	43	68.3	323	2	T22956	hypothetical prote
24	43	68.3	323	2	A31351	probable transmemb
25	43	68.3	464	2	A47655	spliceosome-associ
26	43	68.3	473	2	T08506	trbI protein - Ent
27	43	68.3	496	2	S26402	homeotic protein H
28	43	68.3	533	2	A56110	tyrosine phosphopr
29	43	68.3	684	2	B71379	probable phosphotr
30	43	68.3	700	2	D75508	serine/threonine p
31	43	68.3	802	2	H59434	oligophrenin 1, Rh
32	43	68.3	984	2	A29513	mineralocorticoid
33	42	66.7	148	2	I38881	caudal-type homeot
34	42	66.7	215	2	B75281	peptidyl-tRNA hydr
35	42	66.7	319	2	I38660	melanoma antigen M
36	42	66.7	462	2	E70955	hypothetical prote
37	42	66.7	563	2	T17316	hypothetical prote
38	42	66.7	875	2	T10340	hypothetical prote
39	42	66.7	880	2	T48477	hypothetical prote
40	42	66.7	928	1	RBHU	retinoblastoma-ass
41	42	66.7	1234	2	T30160	hypothetical prote
42	42	66.7	1293	1	A46350	RNA-directed RNA p
43	42	66.7	1607	2	T03022	MAP kinase kinase
44	41	65.1	183	2	F72697	hypothetical prote
45	41	65.1	226	2	S41032	hypothetical prote
46	41	65.1	250	2	F87483	pentapeptide repea
47	41	65.1	304	1	A60472	uracil-DNA glycosy
48	41	65.1	340	1	QQBES6	UL20 protein precu
49	41	65.1	346	2	T32273	hypothetical prote
50	41	65.1	413	2	H87604	hypothetical prote
51	41	65.1	448	2	I50730	yes-associated pro
52	41	65.1	454	2	A56954	yes-associated pro
53	41	65.1	472	2	B56954	yes-associated pro
54	41	65.1	507	2	S52469	SOX9 protein - mou
55	41	65.1	509	2	A55204	transcription fact
56	41	65.1	575	2	JG0181	X11L2 protein - hu
57	41	65.1	681	2	F85062	hypothetical prote
58	41	65.1	731	2	T04455	hypothetical prote
59	41	65.1	757	2	A99561	conserved hypothet
60	41	65.1	759	2	T00875	hypothetical prote
61	41	65.1	845	2	T17291	hypothetical prote
62	41	65.1	902	2	T26775	hypothetical prote
63	41	65.1	920	2	T52426	dynamin-like prote
64	41	65.1	940	2	T00056	hypothetical prote
65	41	65.1	1092	2	H96619	protein T30E16.17
66	41	65.1	1385	2	S61236	major capsid prote
67	41	65.1	1426	2	T30817	homeotic protein C
68	41	65.1	1914	2	T42635	tenascin Y precurs
69	41	65.1	2068	2	A47371	transcription init
70	41	65.1	2649	2	T51023	hypothetical prote

ALIGNMENTS

RESULT 1
A41137
heat shock transcription factor 1 - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: A41137
R;Rabindran, S.K.; Giorgi, G.; Clos, J.; Wu, C.
Proc. Natl. Acad. Sci. U.S.A. 88, 6906-6910, 1991
A;Title: Molecular cloning and expression of a human heat shock factor, HSF1.
A;Reference number: A41137; MUID:91334376; PMID:1871105
A;Accession: A41137
A;Molecule type: mRNA
A;Residues: 1-529 <RAB>
A;Cross-references: UNIPROT:Q00613; GB:M64673; NID:g184402; PIDN:AAA52695.1;
PID:g184403
C;Genetics:
A;Gene: GDB:HSF1
A;Cross-references: GDB:128783; OMIM:140580
A;Map position: 8q24.3-8q24.3
C;Superfamily: tomato heat shock transcription factor HSF8; HSF DNA-binding
domain homology
C;Keywords: DNA binding; leucine zipper; transcription regulation
F;18-124/Domain: HSF DNA-binding domain homology <HSF>

  Query Match   95.2%; Score 60; DB 2; Length 529;
  Best Local Similarity   90.9%; Pred. No. 0.88;
  Matches   10; Conservative   1; Mismatches   0; Indels   0; Gaps   0;

Qy   1 KEEPPAPPQSP 11
              |||||:|||||
Db   298 KEEPPSPPQSP 308

Search completed: November 3, 2005, 09:10:43
Job time : 44 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 3, 2005, 09:10:13 ; Search time 168 Seconds
(without alignments)
27.396 Million cell updates/sec

Title: US-10-810-578-7
Perfect score: 63
Sequence: 1 KEEPPAPPQSP 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	63	100.0	11	9	US-09-951-902-7	Sequence 7, Appli
2	63	100.0	11	16	US-10-810-578-7	Sequence 7, Appli
3	60	95.2	13	18	US-10-862-195-1203	Sequence 1203, Ap
4	60	95.2	305	15	US-10-094-749-1734	Sequence 1734, Ap
5	60	95.2	464	17	US-10-741-600-1343	Sequence 1343, Ap
6	60	95.2	529	14	US-10-046-420-2	Sequence 2, Appli
7	60	95.2	529	17	US-10-732-923-6700	Sequence 6700, Ap
8	60	95.2	529	17	US-10-732-923-6701	Sequence 6701, Ap
9	60	95.2	529	18	US-10-756-149-5144	Sequence 5144, Ap
10	60	95.2	529	18	US-10-984-917-2	Sequence 2, Appli
11	60	95.2	529	18	US-10-996-420-2	Sequence 2, Appli
12	60	95.2	783	14	US-10-100-957A-176	Sequence 176, App
13	57	90.5	11	9	US-09-951-902-8	Sequence 8, Appli
14	57	90.5	11	16	US-10-810-578-8	Sequence 8, Appli
15	54	85.7	382	9	US-09-925-298-484	Sequence 484, App
16	54	85.7	382	14	US-10-102-806-484	Sequence 484, App
17	52	82.5	486	17	US-10-732-923-6451	Sequence 6451, Ap
18	52	82.5	503	17	US-10-732-923-6443	Sequence 6443, Ap
19	52	82.5	525	17	US-10-732-923-6441	Sequence 6441, Ap
20	50	79.4	105	16	US-10-437-963-176405	Sequence 176405,
21	49	77.8	231	16	US-10-437-963-202972	Sequence 202972,
22	48.5	77.0	562	15	US-10-104-047-3214	Sequence 3214, Ap
23	48	76.2	126	16	US-10-425-115-220523	Sequence 220523,
24	48	76.2	172	16	US-10-425-115-343387	Sequence 343387,
25	48	76.2	230	15	US-10-424-599-191232	Sequence 191232,
26	48	76.2	491	17	US-10-732-923-6698	Sequence 6698, Ap
27	48	76.2	1024	16	US-10-437-963-139805	Sequence 139805,
28	47	74.6	19	9	US-09-879-957-170	Sequence 170, App
29	47	74.6	19	16	US-10-807-856-170	Sequence 170, App
30	47	74.6	153	15	US-10-424-599-280543	Sequence 280543,
31	47	74.6	473	16	US-10-437-963-202538	Sequence 202538,
32	47	74.6	537	16	US-10-437-963-188969	Sequence 188969,
33	46	73.0	249	16	US-10-437-963-198871	Sequence 198871,
34	46	73.0	282	15	US-10-389-566-2145	Sequence 2145, Ap
35	46	73.0	295	14	US-10-017-161-2018	Sequence 2018, Ap
36	46	73.0	295	15	US-10-292-798-1664	Sequence 1664, Ap
37	46	73.0	297	16	US-10-437-963-168840	Sequence 168840,
38	46	73.0	308	16	US-10-343-903-1	Sequence 1, Appli
39	46	73.0	388	16	US-10-437-963-152798	Sequence 152798,
40	46	73.0	447	15	US-10-072-012-24	Sequence 24, Appl
41	46	73.0	472	15	US-10-072-012-30	Sequence 30, Appl
42	46	73.0	724	16	US-10-416-898-18	Sequence 18, Appl
43	45	71.4	104	16	US-10-425-115-313062	Sequence 313062,
44	45	71.4	110	15	US-10-424-599-191233	Sequence 191233,
45	45	71.4	111	16	US-10-425-115-286668	Sequence 286668,
46	45	71.4	119	16	US-10-437-963-148420	Sequence 148420,
47	45	71.4	124	16	US-10-437-963-130868	Sequence 130868,
48	45	71.4	132	16	US-10-425-115-197250	Sequence 197250,
49	45	71.4	191	15	US-10-424-599-183002	Sequence 183002,
50	45	71.4	346	20	US-11-008-354-8	Sequence 8, Appli
51	45	71.4	346	20	US-11-107-597-8	Sequence 8, Appli
52	45	71.4	405	16	US-10-437-963-186486	Sequence 186486,

ALIGNMENTS

```
RESULT 1
US-09-951-902-7
; Sequence 7, Application US/09951902
; Patent No. US20020147146A1
; GENERAL INFORMATION:
;  APPLICANT: ELDAR-FINKELMAN, Hagit
;  TITLE OF INVENTION: GLYCOGEN SYNTHASE KINASE-3 INHIBITORS
;  FILE REFERENCE: ELDAR-FINK=1.1B
;  CURRENT APPLICATION NUMBER: US/09/951,902
;  CURRENT FILING DATE:  2001-09-14
;  PRIOR APPLICATION NUMBER: PCT/US01/00123
;  PRIOR FILING DATE: 2001-01-03
;  PRIOR APPLICATION NUMBER: 60/206,115
;  PRIOR FILING DATE: 2000-05-22
;  PRIOR APPLICATION NUMBER: 60/174,308
;  PRIOR FILING DATE: 2000-01-03
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
;   NAME/KEY: misc_feature
;   LOCATION: (10)..(10)
;   OTHER INFORMATION: Ser residue 10 is phosphorylated.
US-09-951-902-7

  Query Match             100.0%;  Score 63;  DB 9;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 0.35;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KEEPPAPPQSP 11
              ||||||||||
Db          1 KEEPPAPPQSP 11


RESULT 3
US-10-862-195-1203
; Sequence 1203, Application US/10862195
; Publication No. US20050164324A1
; GENERAL INFORMATION:
;  APPLICANT: GYGI, STEVEN P.
;  TITLE OF INVENTION: SYSTEMS, METHODS AND KITS FOR CHARACTERIZING
PHOSPHOPROTEOMES
;  FILE REFERENCE: 58890(70207)
;  CURRENT APPLICATION NUMBER: US/10/862,195
;  CURRENT FILING DATE:  2004-06-04
;  PRIOR APPLICATION NUMBER: 60/476,010
;  PRIOR FILING DATE: 2003-06-04
;  NUMBER OF SEQ ID NOS: 2245
;  SOFTWARE: PatentIn version 3.2
```

; SEQ ID NO 1203
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: See specification as filed for preferred embodiments
; OTHER INFORMATION: and description of phosphorylation sites
US-10-862-195-1203

  Query Match 95.2%; Score 60; DB 18; Length 13;
  Best Local Similarity 90.9%; Pred. No. 0.9;
  Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KEEPPAPPQSP 11
      |||||:|||||
Db 2 KEEPPSPPQSP 12

RESULT 4
US-10-094-749-1734
; Sequence 1734, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHIKO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH cDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1734
; LENGTH: 305
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-749-1734

```
  Query Match             95.2%;  Score 60;  DB 15;  Length 305;
  Best Local Similarity   90.9%;  Pred. No. 15;
  Matches   10;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KEEPPAPPQSP 11
              |||||:|||||
Db         87 KEEPPSPPQSP 97


Search completed: November  3, 2005, 09:24:30
Job time : 174 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 3, 2005, 09:02:33 ; Search time 41 Seconds
(without alignments)
20.028 Million cell updates/sec

Title: US-10-810-578-7
Perfect score: 63
Sequence: 1 KEEPPAPPQSP 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	63	100.0	11	4	US-09-951-902-7	Sequence 7, Appli
2	60	95.2	490	4	US-09-949-016-7914	Sequence 7914, Ap
3	60	95.2	529	1	US-08-178-477B-32	Sequence 32, Appl
4	60	95.2	529	3	US-09-304-121-2	Sequence 2, Appli
5	60	95.2	783	4	US-09-513-783A-176	Sequence 176, App
6	57	90.5	11	4	US-09-951-902-8	Sequence 8, Appli
7	47	74.6	19	3	US-08-630-915A-170	Sequence 170, App
8	47	74.6	19	4	US-09-879-957-170	Sequence 170, App
9	45	71.4	564	4	US-09-248-796A-20544	Sequence 20544, A
10	44	69.8	128	4	US-09-489-039A-10886	Sequence 10886, A
11	44	69.8	722	4	US-09-949-016-6909	Sequence 6909, Ap

12	44	69.8	725	4	US-09-949-016-10832	Sequence 10832, A
13	44	69.8	958	4	US-09-706-594-5	Sequence 5, Appli
14	43.5	69.0	25	2	US-08-942-423-25	Sequence 25, Appl
15	43	68.3	15	3	US-08-602-999A-373	Sequence 373, App
16	43	68.3	15	4	US-09-500-124-373	Sequence 373, App
17	43	68.3	35	4	US-09-471-276-1402	Sequence 1402, Ap
18	43	68.3	66	4	US-09-513-999C-5468	Sequence 5468, Ap
19	43	68.3	136	4	US-09-621-976-6751	Sequence 6751, Ap
20	43	68.3	147	2	US-08-756-749C-1	Sequence 1, Appli
21	43	68.3	148	4	US-09-513-999C-5869	Sequence 5869, Ap
22	43	68.3	151	4	US-09-621-976-4549	Sequence 4549, Ap
23	43	68.3	324	4	US-09-949-016-7664	Sequence 7664, Ap
24	43	68.3	505	4	US-09-949-016-6538	Sequence 6538, Ap
25	43	68.3	521	4	US-09-949-016-8809	Sequence 8809, Ap
26	43	68.3	533	4	US-09-949-016-6629	Sequence 6629, Ap
27	43	68.3	545	4	US-09-252-991A-30417	Sequence 30417, A
28	43	68.3	602	4	US-09-949-016-10221	Sequence 10221, A
29	43	68.3	750	4	US-09-949-016-11166	Sequence 11166, A
30	43	68.3	802	4	US-09-949-016-6235	Sequence 6235, Ap
31	43	68.3	984	3	US-08-764-870-15	Sequence 15, Appl
32	43	68.3	984	3	US-08-980-115-15	Sequence 15, Appl
33	43	68.3	984	4	US-09-976-594-127	Sequence 127, App
34	43	68.3	2972	3	US-09-579-181-2	Sequence 2, Appli
35	43	68.3	3118	3	US-09-579-181-1	Sequence 1, Appli
36	43	68.3	4019	4	US-09-854-133-425	Sequence 425, App
37	42	66.7	15	3	US-08-602-999A-423	Sequence 423, App
38	42	66.7	15	4	US-09-500-124-423	Sequence 423, App
39	42	66.7	102	4	US-09-902-540-10936	Sequence 10936, A
40	42	66.7	160	4	US-09-270-767-59046	Sequence 59046, A
41	42	66.7	290	4	US-09-949-016-10385	Sequence 10385, A
42	42	66.7	291	4	US-09-248-796A-20587	Sequence 20587, A
43	42	66.7	294	4	US-09-270-767-36084	Sequence 36084, A
44	42	66.7	294	4	US-09-270-767-51301	Sequence 51301, A
45	42	66.7	319	4	US-09-949-016-8188	Sequence 8188, Ap
46	42	66.7	331	6	5202236-37	Patent No. 5202236
47	42	66.7	331	6	5202236-37	Patent No. 5202236
48	42	66.7	334	6	5202236-3	Patent No. 5202236
49	42	66.7	334	6	5202236-3	Patent No. 5202236
50	42	66.7	348	4	US-09-270-767-31893	Sequence 31893, A
51	42	66.7	348	4	US-09-270-767-47110	Sequence 47110, A
52	42	66.7	415	3	US-09-006-353A-6	Sequence 6, Appli
53	42	66.7	415	4	US-09-573-986-6	Sequence 6, Appli
54	42	66.7	501	4	US-09-252-991A-18409	Sequence 18409, A
55	42	66.7	563	4	US-09-949-016-10801	Sequence 10801, A
56	42	66.7	631	4	US-09-328-352-6860	Sequence 6860, Ap
57	42	66.7	661	4	US-09-949-016-9121	Sequence 9121, Ap
58	42	66.7	795	4	US-09-270-767-43662	Sequence 43662, A
59	42	66.7	836	4	US-09-949-016-10027	Sequence 10027, A
60	42	66.7	836	4	US-09-949-016-10028	Sequence 10028, A
61	42	66.7	928	1	US-08-204-329-1	Sequence 1, Appli
62	42	66.7	928	2	US-08-959-638-8	Sequence 8, Appli
63	42	66.7	928	2	US-08-482-627-5	Sequence 5, Appli
64	42	66.7	928	3	US-08-801-092-4	Sequence 4, Appli
65	42	66.7	928	3	US-08-328-673A-8	Sequence 8, Appli
66	42	66.7	928	3	US-09-315-113-4	Sequence 4, Appli
67	42	66.7	928	4	US-09-354-221-8	Sequence 8, Appli
68	42	66.7	928	5	PCT-US94-10357-2	Sequence 2, Appli

ALIGNMENTS

```
RESULT 1
US-09-951-902-7
; Sequence 7, Application US/09951902
; Patent No. 6780625
; GENERAL INFORMATION:
;  APPLICANT: ELDAR-FINKELMAN, Hagit
;  TITLE OF INVENTION: GLYCOGEN SYNTHASE KINASE-3 INHIBITORS
;  FILE REFERENCE: ELDAR-FINK=1.1B
;  CURRENT APPLICATION NUMBER: US/09/951,902
;  CURRENT FILING DATE:  2001-09-14
;  PRIOR APPLICATION NUMBER: PCT/US01/00123
;  PRIOR FILING DATE: 2001-01-03
;  PRIOR APPLICATION NUMBER: 60/206,115
;  PRIOR FILING DATE: 2000-05-22
;  PRIOR APPLICATION NUMBER: 60/174,308
;  PRIOR FILING DATE: 2000-01-03
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
;   NAME/KEY: misc_feature
;   LOCATION: (10)..(10)
;   OTHER INFORMATION: Ser residue 10 is phosphorylated.
US-09-951-902-7

  Query Match             100.0%;  Score 63;  DB 4;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 0.031;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KEEPPAPPQSP 11
              ||||||||||
Db          1 KEEPPAPPQSP 11


RESULT 2
US-09-949-016-7914
; Sequence 7914, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES
THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
```

; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7914
;   LENGTH: 490
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-7914

  Query Match   95.2%; Score 60; DB 4; Length 490;
  Best Local Similarity   90.9%; Pred. No. 2.5;
  Matches   10; Conservative   1; Mismatches   0; Indels   0; Gaps   0;

Qy   1 KEEPPAPPQSP 11
              |||||:|||||
Db   259 KEEPPSPPQSP 269

RESULT 7
US-08-630-915A-170
; Sequence 170, Application US/08630915A
; Patent No. 6309820
; GENERAL INFORMATION:
;   APPLICANT: SPARKS, Andrew B.
;   APPLICANT: HOFFMAN, No. 6309820h
;   APPLICANT: KAY, Brian K.
;   APPLICANT: FOWLKES, Dana M.
;   APPLICANT: McCONNELL, Stephen J.
;   TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
;   TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
;   TITLE OF INVENTION: USING SAME
;   NUMBER OF SEQUENCES: 227
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Pennie & Edmonds LLP
;   STREET: 1155 Avenue of the Americas
;   CITY: New York
;   STATE: New York
;   COUNTRY: USA
;   ZIP: 10036-2711
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/630,915A
;   FILING DATE: 03-APR-1996
;   CLASSIFICATION: 536
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Misrock, S. Leslie
;   REGISTRATION NUMBER: 18,872
;   REFERENCE/DOCKET NUMBER: 1101-174
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (212) 790-9090

; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 170:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-630-915A-170

Query Match 74.6%; Score 47; DB 3; Length 19;
Best Local Similarity 80.0%; Pred. No. 4.9;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          2 EEPPAPPQSP 11
              |||||||  |
Db          3 EEPPAPPPPP 12
```

Search completed: November 3, 2005, 09:11:26
Job time : 43 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 3, 2005, 08:50:31 ; Search time 165 Seconds
(without alignments)
25.784 Million cell updates/sec

Title: US-10-810-578-7
Perfect score: 63
Sequence: 1 KEEPPAPPQSP 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	63	100.0	11	4	AAG64309	Aag64309 GSK3 pept
2	63	100.0	11	8	ADP47956	Adp47956 GSK-3 inh
3	63	100.0	11	8	ADP47954	Adp47954 Phosphory
4	60	95.2	11	8	ADP47953	Adp47953 Phosphory
5	60	95.2	305	6	ADA54166	Ada54166 Human pro
6	60	95.2	464	8	ADQ39680	Adq39680 Human myo
7	60	95.2	529	2	AAR13503	Aar13503 HSF. 12/2
8	60	95.2	529	2	AAR24948	Aar24948 Sequence
9	60	95.2	529	2	AAW49093	Aaw49093 Human wil

10	60	95.2	529	3	AAY55845	Aay55845 Human hea
11	60	95.2	529	7	ADD48524	Add48524 Human Pro
12	60	95.2	783	3	AAB22939	Aab22939 GFP-HSF1
13	60	95.2	783	5	ABG94502	Abg94502 Protease
14	59	93.7	11	8	ADP47957	Adp47957 GSK-3 inh
15	57	90.5	11	4	AAG64310	Aag64310 GSK3 pept
16	57	90.5	11	8	ADP47955	Adp47955 Phosphory
17	57	90.5	12	8	ADP47962	Adp47962 Phosphory
18	57	90.5	12	8	ADP47964	Adp47964 GSK-3 inh
19	55	87.3	448	7	ADD48522	Add48522 Rat Prote
20	54	85.7	382	3	AAB58776	Aab58776 Breast an
21	50	79.4	13	8	ADP47963	Adp47963 N-myristo
22	48.5	77.0	562	7	ADB65060	Adb65060 Human pro
23	48.5	77.0	562	8	ADR58973	Adr58973 Human Elk
24	48.5	77.0	562	8	ADR58971	Adr58971 Human Elk
25	47	74.6	432	8	ADP44550	Adp44550 Human gly
26	46	73.0	94	4	AAU31792	Aau31792 Novel hum
27	46	73.0	282	8	ADJ50141	Adj50141 Oil-assoc
28	46	73.0	295	7	ADC87211	Adc87211 Human GPC
29	46	73.0	308	5	ABB80594	Abb80594 Human sbg
30	46	73.0	308	5	AAE21157	Aae21157 Human TRI
31	46	73.0	375	4	AAB88570	Aab88570 Human hyd
32	46	73.0	447	5	ABB80595	Abb80595 Human sbg
33	46	73.0	447	5	ADI16488	Adi16488 Human NOV
34	46	73.0	447	8	ADN42144	Adn42144 Human nov
35	46	73.0	471	4	AAM93737	Aam93737 Human pol
36	46	73.0	471	8	ADL31672	Adl31672 Human pro
37	46	73.0	472	5	ADI16494	Adi16494 Human NOV
38	46	73.0	472	8	ADN42150	Adn42150 Human nov
39	46	73.0	572	2	AAW31855	Aaw31855 Mycobacte
40	46	73.0	724	5	ABB83924	Abb83924 Arabidops
41	46	73.0	763	2	AAW31852	Aaw31852 Mycobacte
42	45	71.4	126	4	AAO00517	Aao00517 Human pol
43	45	71.4	195	3	AAB42025	Aab42025 Human ORF
44	45	71.4	389	5	ABP65964	Abp65964 Bifidobac
45	45	71.4	469	4	ABB68765	Abb68765 Drosophil
46	45	71.4	541	5	ABB57066	Abb57066 Mouse isc
47	45	71.4	559	8	ADJ67952	Adj67952 G. stearo
48	45	71.4	559	8	ADJ68164	Adj68164 G. stearo
49	45	71.4	559	8	ADK01242	Adk01242 DNA polym
50	45	71.4	559	8	ADJ79461	Adj79461 G. stearo
51	45	71.4	559	8	ADJ84901	Adj84901 B. steart
52	45	71.4	559	8	ADM77689	Adm77689 DNA polym
53	45	71.4	559	8	ADM66356	Adm66356 G. stearo
54	45	71.4	559	8	ADO04409	Ado04409 B. steart
55	45	71.4	559	8	ADP82486	Adp82486 B. stearo
56	45	71.4	674	4	AAB74208	Aab74208 Protein e
57	45	71.4	674	5	ABB93235	Abb93235 Herbicida
58	45	71.4	674	7	ABR82941	Abr82941 Arabidops
59	45	71.4	681	5	ABB93650	Abb93650 Herbicida
60	45	71.4	830	4	ABB64695	Abb64695 Drosophil
61	45	71.4	907	8	ADS21481	Ads21481 Bacterial
62	44	69.8	59	4	ABG27595	Abg27595 Novel hum
63	44	69.8	65	8	ABO56401	Abo56401 Human gen
64	44	69.8	128	7	ABO64369	Abo64369 Klebsiell
65	44	69.8	135	5	AAE22219	Aae22219 Rodent to
66	44	69.8	185	4	AAU15990	Aau15990 Human nov

ALIGNMENTS

```
RESULT 1
AAG64309
ID   AAG64309 standard; peptide; 11 AA.
XX
AC   AAG64309;
XX
DT   21-SEP-2001  (first entry)
XX
DE   GSK3 peptide inhibitor #2.
XX
KW   Antidiabetic; antidepressant; peptide inhibitor; manic depression;
KW   glycogen synthase kinase-3; GSK3;
KW   non-insulin dependent diabetes mellitus; Alzheimer's disease.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   10
FT                   /label= Phosphoserine
XX
PN   WO200149709-A1.
XX
PD   12-JUL-2001.
XX
PF   03-JAN-2001; 2001WO-US000123.
XX
PR   03-JAN-2000; 2000US-0174308P.
PR   22-MAY-2000; 2000US-0206115P.
XX
PA   (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.
PA   (MCIN/) MCINNIS P A.
XX
PI   Eldar-Finkleman H;
XX
DR   WPI; 2001-451785/48.
XX
PT   Peptide inhibitors of glycogen synthase kinase-3, useful for preventing
PT   and treating non-insulin dependent diabetes mellitus, Alzheimer's disease
PT   and manic depression.
XX
PS   Example 1; Page 30; 49pp; English.
XX
CC   The present invention relates to peptide inhibitors of glycogen synthase
CC   kinase-3 (GSK3). The peptide inhibitors may be used to inhibit the
CC   catalytic activity of GSK3 and treat diseases related to inappropriate
CC   expression and activity of GSK3, e.g. non-insulin dependent (NID)
CC   diabetes mellitus, NID Alzheimer's disease or NID manic depression. In
CC   particular, the peptide inhibitor is administered prophylactically to
CC   prevent NID diabetes mellitus by potentiating insulin signalling in type-
CC   2 diabetics. The present sequence is one such peptide inhibitor for GSK3
XX
SQ   Sequence 11 AA;

  Query Match             100.0%;  Score 63;  DB 4;  Length 11;
```

Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 KEEPPAPPQSP 11
              ||||||||||
Db          1 KEEPPAPPQSP 11
```

RESULT 2
ADP47956
ID ADP47956 standard; peptide; 11 AA.
XX
AC ADP47956;
XX
DT 09-SEP-2004 (first entry)
XX
DE GSK-3 inhibitor peptide, seq id 10.
XX
KW Anorectic; antidiabetic; neuroleptic; antidepressant; cerebroprotective;
KW tranquiliser; vulnerary; neuroprotective; nootropic; anticonvulsant;
KW antiparkinsonian; glycogen synthase kinase-3; GSK-3; insulin signaling;
KW beta-catenin; obesity; non-insulin dependent diabetes mellitus;
KW neurodegenerative disease; psychotic disease; unipolar disorder;
KW bipolar disorder; manic depression; ischaemia; stroke; brain injury;
KW bacterial infection; Alzheimer's disease; Huntington's disease;
KW Parkinson's disease; AIDS associated dementia;
KW amyotrophic lateral sclerosis; AL; multiple sclerosis; schizophrenia.
XX
OS Unidentified.
XX
PN WO2004052404-A2.
XX
PD 24-JUN-2004.
XX
PF 11-DEC-2003; 2003WO-IL001057.
XX
PR 12-DEC-2002; 2002US-0432644P.
PR 27-JUN-2003; 2003US-0482719P.
XX
PA (UYTE-) UNIV TEL AVIV FUTURE TECHNOLOGY DEV LP.
XX
PI Eldar-Finkelman H;
XX
DR WPI; 2004-468713/44.
XX
PT Conjugate useful for treating biological condition e.g., obesity, insulin
PT -dependent condition, neurodegenerative disease or psychotic disease,
PT comprises polypeptide having hydrophobic moiety that inhibits glycogen
PT snythase kinase-3.
XX
PS Example; SEQ ID NO 10; 95pp; English.
XX
CC The invention relates to a conjugate (I) comprising a specific
CC polypeptide and one or more hydrophobic moieties attached to the
CC polypeptide, where (I) is capable of inhibiting an activity of glycogen
CC synthase kinase-3 (GSK-3). Further disclosed is a pharmaceutical
CC composition (II) comprising (I) as an active ingredient. Conjugates of

CC the invention act as inhibitors of GSK-3, stimulators of insulin
CC signaling and Up-regulators of beta-catenin. The conjugate of the
CC invention is useful for treating a biological condition chosen from
CC obesity, non-insulin dependent diabetes mellitus, an insulin-dependent
CC condition, an affective disorder, a neurodegenerative disease or disorder
CC and a psychotic disease or disorder. The affective disorder is chosen
CC from a unipolar disorder and a bipolar disorder. The unipolar disorder is
CC depression. The bipolar disorder is manic depression. The
CC neurodegenerative disorder results from an event chosen from cerebral
CC ischaemia, stroke traumatic brain injury and bacterial infection. The
CC neurodegenerative disorder is a chronic neurodegenerative disorder. The
CC chronic neurodegenerative disorder results from a disease chosen from
CC Alzheimer's disease, Huntington's disease, Parkinson's disease, AIDS
CC associated dementia, amyotrophic lateral sclerosis (AML) and multiple
CC sclerosis. The psychotic disorder is schizophrenia. The pharmaceutical
CC composition is useful for treating biological conditions as mentioned
CC above. The current sequence represents a GSK-3 inhibitor peptide.
XX
SQ Sequence 11 AA;

Query Match 100.0%; Score 63; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KEEPPAPPQSP 11
||||||||||
Db 1 KEEPPAPPQSP 11

RESULT 5
ADA54166
ID ADA54166 standard; protein; 305 AA.
XX
AC ADA54166;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human protein, SEQ ID 1734.
XX
KW Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic;
KW Gene Therapy; human; secretory protein; membrane proteins; cancer;
KW inflammatory disease; osteoporosis; neurological disease.
XX
OS Homo sapiens.
XX
PN EP1293569-A2.
XX
PD 19-MAR-2003.
XX
PF 21-MAR-2002; 2002EP-00006586.
XX
PR 14-SEP-2001; 2001JP-00328381.
PR 24-JAN-2002; 2002US-0350435P.
XX
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.

XX
PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX
DR WPI; 2003-395539/38.
DR N-PSDB; ADA52527.
XX
PT New polynucleotides encoding full-length polypeptides, e.g. secretory
PT and/or membrane proteins, useful for developing medicines for diseases in
PT which the gene is involved, or as target molecules for gene therapy.
XX
PS Claim 14; SEQ ID NO 1734; 205pp; English.
XX
CC The present invention relates to novel human secretory or membrane
CC proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-
CC ADA54071). The coding sequences are useful in the gene therapy of
CC diseases caused by abnormalities of the proteins, e.g. cancer,
CC inflammatory diseases, osteoporosis or neurological disease.
XX
SQ Sequence 305 AA;

Query Match 95.2%; Score 60; DB 6; Length 305;
Best Local Similarity 90.9%; Pred. No. 6.9;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 KEEPPAPPQSP 11
              |||||:|||||
Db         87 KEEPPSPPQSP 97
```

Search completed: November 3, 2005, 09:07:08
Job time : 179 secs